EAST Search History

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
S1	1	"6110672".pn.	US-PGPUB; USPAT	OR	ON	2006/08/09 10:37
S2	2081	(scn3a or (type adj III)) and sodium and channel	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2006/08/09 10:38
S3	1307	(scn3a or (type adj III)) and sodium and channel and human and brain	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2006/08/09 10:38
S4	1088	(scn3a or (type adj III)) and sodium and channel and human and brain and (genomic or cdna)	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2006/08/09 10:39
S5	60	(scn3a or (type adj III)) and sodium and channel and human and brain and (genomic or cdna) and @py<"2001"	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2006/08/09 11:00
S6	27	S4 and (chen.in. or dale.in. or romanos.in. or whitaker.in. or xie. in. or clare.in.)	US-PGPUB; USPAT; EPO; DERWENT	OR	ON	2006/08/09 11:01

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OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 08:00:38 ; Search time 1488 Seconds
                                            (without alignments)
                                            11458.026 Million cell updates/sec

Title: US-10-664-422A-65
Perfect score: 9110.8
Sequence: 1 accatagagtgaatctcaga..........aaattatataaggtggctaa 9112

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
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                9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                10: /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5033.4	55.2	5106	3	US-09-976-594-1104	Sequence 1104, Ap
2	4203	46.1	6332	3	US-09-949-016-5117	Sequence 5117, Ap
3	3419	37.5	6348	3	US-09-976-594-756	Sequence 756, App
4	3419	37.5	6348	3	US-09-919-039-366	Sequence 366, App
5	3419	37.5	6371	3	US-08-836-325-13	Sequence 13, Appl
6	3419	37.5	6371	3	US-09-457-571-13	Sequence 13, Appl
7	3386	37.2	6404	3	US-08-836-325-14	Sequence 14, Appl
8	3386	37.2	6404	3	US-09-457-571-14	Sequence 14, Appl
9	3164.6	34.7	6452	3	US-08-836-325-9	Sequence 9, Appli
10	3164.6	34.7	6452	3	US-09-457-571-9	Sequence 9, Appli
11	2642.4	29.0	6882	3	US-09-949-016-4205	Sequence 4205, Ap
12	2640.4	29.0	6556	3	US-09-024-020B-7	Sequence 7, Appli

13	2640.4	29.0	6556	3	US-09-425-043-7	Sequence 7, Appli
14	2633.2	28.9	5977	3	US-09-024-020B-1	Sequence 1, Appli
15	2633.2	28.9	5977	3	US-09-425-043-1	Sequence 1, Appli
16	2610.4	28.7	6586	3	US-09-024-020B-43	Sequence 43, Appl
17	2610.4	28.7	6586	3	US-09-425-043-43	Sequence 43, Appl
18	2604.8	28.6	6007	3	US-09-024-020B-2	Sequence 2, Appli
19	2604.8	28.6	6007	3	US-09-425-043-2	Sequence 2, Appli
20	2570.4	28.2	6826	3	US-09-024-020B-8	Sequence 8, Appli
21	2570.4	28.2	6826	3	US-09-425-043-8	Sequence 8, Appli
22	1921.2	21.1	6048	3	US-09-514-907A-1	Sequence 1, Appli
23	1921.2	21.1	6048	3	US-09-896-994-1	Sequence 1, Appli
24	1919.6	21.1	6048	3	US-09-634-920-3	Sequence 3, Appli
25	1919.6	21.1	6048	3	US-09-840-125-3	Sequence 3, Appli
26	1812.6	19.9	3033	3	US-08-836-325-1	Sequence 1, Appli
27	1812.6	19.9	3033	3	US-09-457-571-1	Sequence 1, Appli
28	1701.4	18.7	5874	3	US-08-843-417-9	Sequence 9, Appli
29	1701.4	18.7	5874	3	US-09-527-013-9	Sequence 9, Appli
30	1620.8	17.8	6527	3	US-08-669-656A-7	Sequence 7, Appli
31	1616.2	17.7	6344	3	US-08-843-417-1	Sequence 1, Appli
32	1616.2	17.7	6344	3	US-09-527-013-1	Sequence 1, Appli
33	1612.8	17.7	6524	3	US-08-669-656A-1	Sequence 1, Appli
34	1360.6	14.9	5482	3	US-09-920-653B-2	Sequence 2, Appli
35	1307.2	14.3	7052	3	US-08-669-656A-5	Sequence 5, Appli
36	1165.4	12.8	2490	3	US-09-976-594-361	Sequence 361, App
37	1132.8	12.4	99830	3	US-09-949-016-16859	Sequence 16859, A
38	1107.4	12.2	5822	3	US-09-354-147C-4	Sequence 4, Appli
39	1091.8	12.0	5860	3	US-09-354-147C-41	Sequence 41, Appl
40	1084.8	11.9	5875	3	US-09-354-147C-1	Sequence 1, Appli
41	908.8	10.0	6519	2	US-08-808-793-24	Sequence 24, Appl
42	904.6	9.9	930	3	US-08-605-284B-21	Sequence 21, Appl
43	893.8	9.8	930	3	US-08-605-284B-1	Sequence 1, Appli
44	892.2	9.8	930	3	US-08-605-284B-3	Sequence 3, Appli
45	855.4	9.4	930	3	US-08-605-284B-2	Sequence 2, Appli

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 OM nucleic - nucleic search, using sw model

 Run on:          August  5, 2006, 08:03:03 ; Search time 4993 Seconds
                                             (without alignments)
                                             12724.039 Million cell updates/sec


 Title:          US-10-664-422A-65
 Perfect score:  9110.8
 Sequence:       1 accatagagtgaatctcaga..........aaattatataaggtggctaa 9112


 Scoring table:  IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0


 Searched:       5244920 seqs, 3486124231 residues


 Total number of hits satisfying chosen parameters:      10489840


 Minimum DB seq length: 0
 Maximum DB seq length: 2000000000


 Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries


 Database :      N_Geneseq_8:*
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                 2:  geneseqn1990s:*
                 3:  geneseqn2000s:*
                 4:  geneseqn2001as:*
                 5:  geneseqn2001bs:*
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                 7:  geneseqn2002bs:*
                 8:  geneseqn2003as:*
                 9:  geneseqn2003bs:*
                 10:  geneseqn2003cs:*
                 11:  geneseqn2003ds:*
                 12:  geneseqn2004as:*
                 13:  geneseqn2004bs:*
                 14:  geneseqn2005s:*
                 15:  geneseqn2006s:*


         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.
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                                    SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	9110.8	100.0	9112	5	AAH55823	Aah55823 Human adu
2	9075.6	99.6	9112	5	AAH55824	Aah55824 Human neo
3	8723.2	95.7	8976	12	ADL06499	Adl06499 Human tum
4	8723.2	95.7	8976	14	AEA44249	Aea44249 Human SCN
5	8563	94.0	9120	12	ADK81761	Adk81761 Human Nav
6	8563	94.0	9123	6	ABL39690	Abl39690 Human sod
7	8563	94.0	9123	13	ADP79544	Adp79544 Human sod

8	8563	94.0	9123	14	AEA44247	Aea44247 Human sod
9	6395	70.2	6599	13	ADP79542	Adp79542 Human sod
10	6393.4	70.2	6599	10	ADB78650	Adb78650 Human ion
11	6393.4	70.2	6599	10	ADB78648	Adb78648 Human ion
12	6393.4	70.2	6599	10	ADB78647	Adb78647 Human ion
13	6379	70.0	6596	10	ADB78646	Adb78646 Human ion
14	5694.2	62.5	6057	13	ADP79540	Adp79540 Human sod
15	5657.8	62.1	6003	14	ADV42845	Adv42845 Human psy
16	5169.8	56.7	6822	6	ABK63697	Abk63697 Rat seque
17	5169.8	56.7	6822	14	AEA44251	Aea44251 Rat sodiu
18	5033.4	55.2	5106	12	ADL13375	Adl13375 Human ste
19	4778	52.4	6071	14	AEA44246	Aea44246 Murine so
20	4738.8	52.0	5940	14	AEA44244	Aea44244 Murine so
21	4279.8	47.0	8292	10	ADC46961	Adc46961 Human SCN
22	4271.2	46.9	7028	6	ABZ35519	Abz35519 Human gen
23	4271.2	46.9	8349	5	AAH55793	Aah55793 Human adu
24	4271.2	46.9	8349	5	AAH55794	Aah55794 Human neo
25	4215.4	46.3	6328	10	ADB78643	Adb78643 Human ion
26	4213.8	46.3	6328	10	ADB78644	Adb78644 Human ion
27	4213.8	46.3	6328	10	ADB78642	Adb78642 Human ion
28	4213.8	46.3	6328	10	ADA19378	Ada19378 Human ins
29	4213.8	46.3	6328	13	ADS52206	Ads52206 Human sod
30	4213.8	46.3	6328	14	ADY27081	Ady27081 Human SCN
31	4213.8	46.3	6328	14	ADY27080	Ady27080 Human SCN
32	4213.8	46.3	6328	14	ADY27078	Ady27078 Human SCN
33	4213.8	46.3	6328	14	ADY27079	Ady27079 Human SCN
34	4213.8	46.3	6328	14	ADY27076	Ady27076 Human SCN
35	4213.8	46.3	6328	14	ADY27077	Ady27077 Human SCN
36	4213.8	46.3	6328	14	ADY27075	Ady27075 Human SCN
37	4108.8	45.1	6018	6	ABQ79201	Abq79201 Human GEF
38	4108.8	45.1	6018	14	ADV42844	Adv42844 Human psy
39	4084	44.8	4153	12	ADL06498	Adl06498 Human tum
40	3987.2	43.8	8131	6	ABL39689	Abl39689 Human sod
41	3987.2	43.8	8131	13	ADS16301	Ads16301 Human vol
42	3955	43.4	8381	6	ABK98844	Abk98844 Human sod
43	3953.4	43.4	8381	6	ABK98846	Abk98846 Human sod
44	3953.4	43.4	8381	6	ABK98924	Abk98924 Human sod
45	3953.4	43.4	8381	6	ABK98847	Abk98847 Human sod

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OM nucleic - nucleic search, using sw model

Run on: August 5, 2006, 08:05:13 ; Search time 9584 Seconds
                                            (without alignments)
                                            11682.485 Million cell updates/sec

Title: US-10-664-422A-65
Perfect score: 9110.8
Sequence: 1 accatagagtgaatctcaga..........aaattatataaggtggctaa 9112

Scoring table: IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched: 18892170 seqs, 6143817638 residues

Total number of hits satisfying chosen parameters: 37784340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA_Main:*
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                3: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                4: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
                5: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
                6: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
                7: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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                9: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
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                11: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
                12: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
                13: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
                14: /EMC_Celerra_SIDS3/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                    %
Result   Query
  No.   Score Match Length DB ID   Description
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       1 9110.8 100.0   9112 8 US-10-664-422-65   Sequence 65, Appl
       2 9110.8 100.0   9112 8 US-10-664-423-65   Sequence 65, Appl
       3 9110.8 100.0   9112 9 US-10-664-603-65   Sequence 65, Appl
       4 9075.6 99.6   9112 8 US-10-664-422-66   Sequence 66, Appl
       5 9075.6 99.6   9112 8 US-10-664-423-66   Sequence 66, Appl
       6 9075.6 99.6   9112 9 US-10-664-603-66   Sequence 66, Appl

7	8723.2	95.7	8976	9	US-10-643-795A-79	Sequence 79, Appl
8	8723.2	95.7	8976	10	US-10-948-518-79	Sequence 79, Appl
9	8723.2	95.7	8976	12	US-10-960-414-327	Sequence 327, App
10	6393.4	70.2	6599	10	US-10-482-834A-18	Sequence 18, Appl
11	6393.4	70.2	6599	10	US-10-482-834A-19	Sequence 19, Appl
12	6393.4	70.2	6599	10	US-10-482-834A-21	Sequence 21, Appl
13	6379	70.0	6596	10	US-10-482-834A-17	Sequence 17, Appl
14	5169.8	56.7	6822	3	US-09-917-800A-1604	Sequence 1604, Ap
15	5168.2	56.7	6822	16	US-11-136-527-259	Sequence 259, App
16	4271.2	46.9	7028	7	US-10-101-510-630	Sequence 630, App
17	4271.2	46.9	8349	8	US-10-664-422-33	Sequence 33, Appl
18	4271.2	46.9	8349	8	US-10-664-422-34	Sequence 34, Appl
19	4271.2	46.9	8349	8	US-10-664-423-33	Sequence 33, Appl
20	4271.2	46.9	8349	8	US-10-664-423-34	Sequence 34, Appl
21	4271.2	46.9	8349	9	US-10-664-603-33	Sequence 33, Appl
22	4271.2	46.9	8349	9	US-10-664-603-34	Sequence 34, Appl
23	4215.4	46.3	6328	10	US-10-482-834A-14	Sequence 14, Appl
24	4213.8	46.3	6328	6	US-10-161-803-60	Sequence 60, Appl
25	4213.8	46.3	6328	10	US-10-482-834A-13	Sequence 13, Appl
26	4213.8	46.3	6328	10	US-10-482-834A-15	Sequence 15, Appl
27	4084	44.8	4153	9	US-10-643-795A-78	Sequence 78, Appl
28	4084	44.8	4153	10	US-10-948-518-78	Sequence 78, Appl
29	3987.2	43.8	8131	9	US-10-377-139-13	Sequence 13, Appl
30	3955	43.4	8381	8	US-10-451-126A-7	Sequence 7, Appli
31	3953.4	43.4	8381	8	US-10-451-126A-9	Sequence 9, Appli
32	3953.4	43.4	8381	8	US-10-451-126A-11	Sequence 11, Appl
33	3953.4	43.4	8381	8	US-10-451-126A-89	Sequence 89, Appl
34	3953.4	43.4	8381	9	US-10-806-899-4	Sequence 4, Appli
35	3951.8	43.4	8381	8	US-10-451-126A-1	Sequence 1, Appli
36	3951.8	43.4	8381	8	US-10-451-126A-3	Sequence 3, Appli
37	3951.8	43.4	8381	8	US-10-451-126A-5	Sequence 5, Appli
38	3951.8	43.4	8381	8	US-10-451-126A-8	Sequence 8, Appli
39	3951.8	43.4	8381	9	US-10-806-899-1	Sequence 1, Appli
40	3951.8	43.4	8381	9	US-10-806-899-2	Sequence 2, Appli
41	3951.8	43.4	8381	9	US-10-806-899-3	Sequence 3, Appli
42	3951.8	43.4	8381	9	US-10-806-899-5	Sequence 5, Appli
43	3951.8	43.4	8381	9	US-10-806-899-6	Sequence 6, Appli
44	3951.8	43.4	8381	9	US-10-806-899-7	Sequence 7, Appli
45	3951.8	43.4	8381	9	US-10-806-899-8	Sequence 8, Appli

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OM nucleic - nucleic search, using sw model

Run on:            August  5, 2006, 08:29:13 ; Search time 1292 Seconds
                                              (without alignments)
                                              11170.206 Million cell updates/sec

Title:             US-10-664-422A-65
Perfect score:     9110.8
Sequence:          1 accatagagtgaatctcaga..........aaattatataaggtggctaa 9112

Scoring table:     IDENTITY_NUC
                   Gapop 10.0 , Gapext 1.0

Searched:          2193277 seqs, 791917567 residues

Total number of hits satisfying chosen parameters:       4386554

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :         Published_Applications_NA_New:*
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                   3:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                   4:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                   5:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                   6:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                   7:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq:*
                   8:  /EMC_Celerra_SIDS3/ptodata/1/pubpna/US11_NEW_PUB.seq1:*
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          Pred. No. is the number of results predicted by chance to have a
          score greater than or equal to the score of the result being printed,
          and is derived by analysis of the total score distribution.

                                  SUMMARIES
                      %
Result             Query
   No.    Score    Match Length DB  ID                       Description
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      1    8563     94.0   9123  8  US-11-266-748A-56739      Sequence 56739, A
      2   6393.4    70.2   6599  8  US-11-263-326-106         Sequence 106, App
      3   6393.4    70.2   6599  8  US-11-263-326-107         Sequence 107, App
      4   6393.4    70.2   6599  8  US-11-263-326-109         Sequence 109, App
      5   6379      70.0   6596  8  US-11-263-326-105         Sequence 105, App
      6   5657.8    62.1   6003  8  US-11-313-450-5           Sequence 5, Appli
      7   4279.8    47.0   8292  6  US-10-501-814-2           Sequence 2, Appli
      8   4215.4    46.3   6328  8  US-11-263-326-102         Sequence 102, App
      9   4213.8    46.3   6328  8  US-11-263-326-101         Sequence 101, App
     10   4213.8    46.3   6328  8  US-11-263-326-103         Sequence 103, App
     11   4213.8    46.3   6328  8  US-11-263-326-146         Sequence 146, App
     12   4213.8    46.3   6328  8  US-11-263-326-147         Sequence 147, App
     13   4213.8    46.3   6328  8  US-11-263-326-148         Sequence 148, App
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14	4213.8	46.3	6328	8	US-11-263-326-149	Sequence 149, App
15	4213.8	46.3	6328	8	US-11-263-326-150	Sequence 150, App
16	4213.8	46.3	6328	8	US-11-263-326-151	Sequence 151, App
17	4213.8	46.3	6328	8	US-11-263-326-152	Sequence 152, App
18	4108.8	45.1	6018	8	US-11-313-450-3	Sequence 3, Appli
19	3955	43.4	8381	8	US-11-263-326-7	Sequence 7, Appli
20	3953.4	43.4	8381	8	US-11-263-326-9	Sequence 9, Appli
21	3953.4	43.4	8381	8	US-11-263-326-11	Sequence 11, Appl
22	3953.4	43.4	8381	8	US-11-263-326-143	Sequence 143, App
23	3953.4	43.4	8381	8	US-11-263-326-144	Sequence 144, App
24	3951.8	43.4	8381	8	US-11-263-326-1	Sequence 1, Appli
25	3951.8	43.4	8381	8	US-11-263-326-3	Sequence 3, Appli
26	3951.8	43.4	8381	8	US-11-263-326-5	Sequence 5, Appli
27	3951.8	43.4	8381	8	US-11-263-326-8	Sequence 8, Appli
28	3951.8	43.4	8381	8	US-11-263-326-91	Sequence 91, Appl
29	3951.8	43.4	8381	8	US-11-263-326-92	Sequence 92, Appl
30	3951.8	43.4	8381	8	US-11-263-326-93	Sequence 93, Appl
31	3951.8	43.4	8381	8	US-11-263-326-96	Sequence 96, Appl
32	3951.8	43.4	8381	8	US-11-263-326-97	Sequence 97, Appl
33	3951.8	43.4	8381	8	US-11-263-326-108	Sequence 108, App
34	3951.8	43.4	8381	8	US-11-263-326-136	Sequence 136, App
35	3951.8	43.4	8381	8	US-11-263-326-137	Sequence 137, App
36	3951.8	43.4	8381	8	US-11-263-326-138	Sequence 138, App
37	3951.8	43.4	8381	8	US-11-263-326-139	Sequence 139, App
38	3951.8	43.4	8381	8	US-11-263-326-140	Sequence 140, App
39	3951.8	43.4	8381	8	US-11-263-326-141	Sequence 141, App
40	3951.8	43.4	8381	8	US-11-263-326-142	Sequence 142, App
41	3941.4	43.3	8380	8	US-11-263-326-89	Sequence 89, Appl
42	3937	43.2	8377	8	US-11-263-326-95	Sequence 95, Appl
43	3936.4	43.2	8388	8	US-11-263-326-94	Sequence 94, Appl
44	3924.6	43.1	8370	8	US-11-263-326-90	Sequence 90, Appl
45	3815.2	41.9	5997	8	US-11-313-450-1	Sequence 1, Appli

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OM nucleic - nucleic search, using sw model

Run on: June 21, 2006, 11:33:43 ; Search time 49169 Seconds
                                           (without alignments)
                                           11850.737 Million cell updates/sec

Title: US-10-664-422A-65
Perfect score: 9110.8
Sequence: 1 accatagagtgaatctcaga..........aaattatataaggtggctaa 9112

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_env:*
                 2: gb_pat:*
                 3: gb_ph:*
                 4: gb_pl:*
                 5: gb_pr:*
                 6: gb_ro:*
                 7: gb_sts:*
                 8: gb_sy:*
                 9: gb_un:*
                 10: gb_vi:*
                 11: gb_ov:*
                 12: gb_htg:*
                 13: gb_in:*
                 14: gb_om:*
                 15: gb_ba:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	9110.8	100.0	9112	2	AX164235	AX164235 Sequence
2	9075.6	99.6	9112	2	AX164236	AX164236 Sequence
3	8723.2	95.7	8976	5	AF225986	AF225986 Homo sapi
4	8563	94.0	9123	2	BD094361	BD094361 Sodium ch
5	8563	94.0	9123	2	BD105258	BD105258 Sodium ch
6	8563	94.0	9123	5	AF225987	AF225987 Homo sapi
7	6395	70.2	6599	5	HSA251507	AJ251507 Homo sapi

8	5169.8	56.7	6822	2	AX401928	AX401928 Sequence
9	5169.8	56.7	6822	6	RNSCIII	Y00766 Rat mRNA fo
10	5033.4	55.2	5106	2	AR448401	AR448401 Sequence
11	4279.8	47.0	8292	2	AX805577	AX805577 Sequence
12	4271.2	46.9	8349	2	AX164203	AX164203 Sequence
13	4271.2	46.9	8349	2	AX164204	AX164204 Sequence
14	4213.8	46.3	6328	5	HUMHBAX	M94055 Human volta
15	4150.2	45.6	4183	5	AB037777	AB037777 Homo sapi
16	4117.6	45.2	4153	5	AF035686	AF035686 Homo sapi
17	4108.8	45.1	6018	2	BD144094	BD144094 GEFS + re
18	4084	44.8	4153	5	AF035685	AF035685 Homo sapi
19	3987.2	43.8	8131	2	BD094360	BD094360 Sodium ch
20	3987.2	43.8	8131	2	BD105257	BD105257 Sodium ch
21	3987.2	43.8	8131	5	AF225985	AF225985 Homo sapi
22	3949.6	43.4	8378	2	AX164171	AX164171 Sequence
23	3914.4	43.0	8378	2	AX164172	AX164172 Sequence
24	3884.6	42.6	8553	6	RNSCPIIR	X03639 Rat brain m
25	3875.8	42.5	8552	6	RATNACHII	M22254 Rattus norv
26	3870.2	42.5	5946	5	AB098335	AB098335 Homo sapi
27	3825	42.0	3975	2	AX164268	AX164268 Sequence
28	3824.4	42.0	6046	5	AY043484	AY043484 Homo sapi
29	3819.2	41.9	5997	5	AB093549	AB093549 Homo sapi
30	3818.4	41.9	5997	2	AX391130	AX391130 Sequence
31	3815.2	41.9	5997	2	DD182524	DD182524 Mutations
c 32	3803.8	41.8	168493	5	AC013463	AC013463 Homo sapi
33	3786.2	41.6	6030	5	AB093548	AB093548 Homo sapi
34	3785.4	41.5	6030	2	AX391140	AX391140 Sequence
35	3784.8	41.5	5889	2	AX391132	AX391132 Sequence
36	3784.6	41.5	6030	2	BD144093	BD144093 GEFS + re
37	3777.8	41.5	6027	2	AX709969	AX709969 Sequence
38	3751.8	41.2	5922	2	AX391142	AX391142 Sequence
39	3740	41.1	8398	6	RNSCPIR	X03638 Rat brain m
40	3740	41.1	8399	6	RATNACHI	M22253 Rattus norv
41	3436.8	37.7	8378	11	AF123593	AF123593 Cynops py
42	3419	37.5	6348	2	AR448089	AR448089 Sequence
43	3419	37.5	6348	2	AR531777	AR531777 Sequence
44	3419	37.5	6371	2	AR107905	AR107905 Sequence
45	3419	37.5	6371	2	AR483560	AR483560 Sequence

```
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OM nucleic - nucleic search, using sw model

Run on:           June 21, 2006, 12:57:28 ; Search time 38005 Seconds
                                            (without alignments)
                                            13407.103 Million cell updates/sec


Title:            US-10-664-422A-65
Perfect score:    9110.8
Sequence:         1 accatagagtgaatctcaga..........aaattatataaggtggctaa 9112

Scoring table:    IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched:         48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters:        96473596

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        EST:*
                  1:  gb_est1:*
                  2:  gb_est3:*
                  3:  gb_est4:*
                  4:  gb_est5:*
                  5:  gb_est6:*
                  6:  gb_htc:*
                  7:  gb_est2:*
                  8:  gb_est7:*
                  9:  gb_est8:*
                  10:  gb_est9:*
                  11:  gb_gss1:*
                  12:  gb_gss2:*
                  13:  gb_gss3:*
                  14:  gb_gss4:*

       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.
```

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	3577.6	39.3	5994	14	DQ050103	DQ050103 Homo sapi
2	3000	32.9	5963	14	DQ050104	DQ050104 Pan trogl
3	2274.2	25.0	5943	14	AY416499	AY416499 Homo sapi
4	2019.4	22.2	5710	14	AY416500	AY416500 Pan trogl
5	1986.8	21.8	5666	14	AY416501	AY416501 Mus muscu
6	1915.6	21.0	8452	6	AK147254	AK147254 Mus muscu
7	1915.6	21.0	8452	6	AK147517	AK147517 Mus muscu
8	1848.8	20.3	4675	6	AK083220	AK083220 Mus muscu

	9	1766.4	19.4	6096	14	DQ052007	DQ052007 Homo sapi
	10	1616	17.7	5933	6	AK157866	AK157866 Mus muscu
	11	1547	17.0	5751	14	DQ052008	DQ052008 Pan trogl
	12	1440	15.8	5046	14	DQ042904	DQ042904 Homo sapi
	13	1320.8	14.5	2306	6	AK141113	AK141113 Mus muscu
	14	1239	13.6	5046	14	DQ042905	DQ042905 Pan trogl
	15	1035.8	11.4	3043	6	AK148881	AK148881 Mus muscu
	16	1016.6	11.2	1689	6	AK134744	AK134744 Mus muscu
	17	939.6	10.3	2802	6	AK032187	AK032187 Mus muscu
	18	856.2	9.4	870	3	BQ941318	BQ941318 AGENCOURT
	19	773.8	8.5	2527	6	AK158609	AK158609 Mus muscu
	20	764.4	8.4	814	8	CX165145	CX165145 HESC2_25_
	21	733	8.0	1762	6	AK142068	AK142068 Mus muscu
c	22	719.2	7.9	807	5	CD623433	CD623433 55050937J
	23	700.6	7.7	928	3	BQ715936	BQ715936 AGENCOURT
	24	681	7.5	799	14	CT410732	CT410732 Sus scrof
	25	675.4	7.4	881	12	CC542775	CC542775 CH240_424
	26	666.4	7.3	801	5	CJ468512	CJ468512 CJ468512
	27	660	7.2	735	2	BI488967	BI488967 603021693
c	28	654.2	7.2	682	3	BM681920	BM681920 UI-E-EO1-
	29	649.2	7.1	785	9	CX562753	CX562753 UI-M-IB0-
	30	632.4	6.9	716	5	CD623432	CD623432 55050937H
	31	632	6.9	938	14	CT220677	CT220677 Sus scrof
	32	631.6	6.9	768	4	CB520657	CB520657 UI-M-GI0-
	33	625.8	6.9	689	7	BF347024	BF347024 602021819
	34	617	6.8	673	8	CR538717	CR538717 DKFZp459P
	35	615	6.8	2343	6	AK048407	AK048407 Mus muscu
	36	614.6	6.7	637	1	AV702029	AV702029 AV702029
	37	614.4	6.7	763	5	CJ465576	CJ465576 CJ465576
	38	614	6.7	873	7	BF527027	BF527027 602039918
	39	613.4	6.7	616	3	BM728972	BM728972 UI-E-EO1-
	40	606.8	6.7	972	8	CN646516	CN646516 ILLUMIGEN
	41	605	6.6	704	10	DT895022	DT895022 1478017 M
	42	603.2	6.6	753	5	CJ465757	CJ465757 CJ465757
	43	594.8	6.5	775	8	CX238600	CX238600 NMA06245
c	44	594.6	6.5	761	13	DU437968	DU437968 109842100
	45	594.2	6.5	671	9	DA224704	DA224704 DA224704